

FIG. 2

 ${\tt TGAGTCA} {\tt CACCCTGAAACACGGCTCTCTTCCTGTCAGGACTGAGTCAGGTAGAAGAGTC\underline{GATAA} {\tt CACCTGATCAAGGAAAAG}$ -91 GAAGGCACAGCGGAGCGCAGAGTGAGAACTCCCAGCGGCGAGGCGCCGGGCAGCCCTGCAGCGGCGGACCGCGCCGGCCTGGCC -1 M P A L W L S C Y L C F S L L L P A A R A T S G R E V C D C 30 AACGGGAAGTCCAGGCAATGCATCTTTGACCAGGAACTTCACAAACAGGACATGGAATGGATTCCGCTGCCTCAACTGCAATGACAACACT 180 NGKSRQCIFDQELHKQTGNGFRCLNCNDNT GATGGCATCCACTGCGAGAGGTGCAAGGCAGGATTTTACCGACAGAGAGAAAGGGACCGCTGTTTACCCTGCAATTGTAACTCTAAAGGT 270 D G I H C E R C K A G F Y R Q R E R D R C L P C N C N S K G 90 TCTCTTAGCGCTCGATGTGACAACTCTGGACGGTGCAGCTGTAAGCCAGGTGTGACAGGAGACAGGTGTGACCGATGTCTGCCCGGCTTC 360 S L S A R C D N S G R C S C K P G V T G D R C D R C L P G F 120 CACACTCACTGATGCTGGGTGCGCCCAAGACCAAAGGCTGCTAGACTCCAAGTGTGACCCAGCTGGCATCTCAGGGCCCTGT 450 H T L T D A G C A Q D Q R L L D S K C D C D P A G I S G P C GACTCAGGCCGCTGTGTCTGCAAGCCGGCTGTCACTGGAGAGCGCTGTGATAGGTGTCGACCAGGTTACTATCACCTGGATGGGGGAAAC 540 D S G R C V C K P A V T G E R C D R C R P G Y Y H L D G G N 180 CCTCAGGGCTGTACCCAGTGTTTTTGCTATGGGCATTCCGCCAGCTGCCACAGCTCTGGGGACTACAGTGTCCATAAAATCATCTCTGCC 630 QGCTQCFCYGHSA|SCHSSGDYSVHKIISA 210 dom. IV TTCTACAGATGTTGATGGCTGGAAGGCTGTCCAAAGAAACGGGTCTCCTGCAAAGCTCCAGTGGTCACAGCGCCCATCGGGATATATTT 720 FQDVDGWKAVQR<mark>NGS</mark>PAKLQWSQRHRDIF AGCTTAGCACGACGATCAGACCCTGTCTATTTTGTAGCTCCTGCCAAATTTCTTGGGAATCAACAGGTGAGCTACGGGCAAAGCCTATCT 810 鮮ARRSDPVYFVAPAKFLGNQQVSYGQSLS 270 ${\tt TTT}_{\P^{\bullet}}{\tt CTACCGTGTGGATAGGGGAGCAGCCATCTGCCCATGACGTGATCTGGAAGGTGCTGGTCTACGGATCACAGCTCCCTTG} {\tt 900}$ Y R V D R G G R H P S A H D V I L E G A G L R I T A P L 300 ATGCACTTAGCAAGACACTGCCTTGTGGGATCACCAAGACTTACACATTCAGATTAAATGAACATCCAAGCAGTAATTGGAGCCCCCAG 990 M PL S K T L P C G I T K T Y T F R L N E H P S S N W S P Q ŚÜYFEYRRLLR<u>NLT</u>ALRIRATYGEYSTGYI 360 GACAACGTGACCTTGATTTCAGCCCGCCCCGTTTCTGGAGCCCCAGCGCCCCTGGGTTGAACAATGTGTATGCCCTGTTGGCTACAAGGGG 1170 <u>щі V T</u> L I S A R P V S G A P A P W V E Q C V C P V G Y K G 390 DOM. TIT CAGTTCTGCCAGGATTGTGCTTCCGGCTACAAAAGAGATTCAGCCAGACTGGGACCTTTTTGGCACCTGTATTCCATGTAACTGCCAAGGG 1260 Q F C Q D C A S G Y K R D S A R L G P F G T C I P C N C Q G 420 GGAGGGCCTGCGATCCAGACACAGGAGACTGTTACTCAGGGGATGAGAACCCTGACATCCCTGAGTGTGCTGACTGCCCCATTGGTTTC 1350 $\texttt{G} \ \ \texttt{G} \ \ \texttt{A} \ \ \texttt{C} \ \ \texttt{D} \ \ \texttt{P} \ \ \texttt{D} \ \ \texttt{C} \ \ \texttt{P} \ \ \texttt{I} \ \ \texttt{G} \ \ \texttt{F} \quad \ \ \, \texttt{450}$ TACAACGATCCACAAGACCCCCGCAGCTGCAGCCGTGCCCCTGTCGCAATGGGTTCAGCTGCTGCTGATGCCTGAGACAGAGAGGGGGTG 1440 Y N D P Q D P R S C K P C P C R N G F S C S V M P E T E E V 480 GTGTGCAATAACTGCCCCCAGGGTGTCACTGGTGCCCGCTGTGAGCTCTGTGCTGATGGCTATTTTGGGGACCCCTTCGGGGAACGTGGC 1530 V C N N C P Q G V T G A R C E L C A D G Y F G D P F G E R G 510 P V R P C Q P C Q C N N N V D P S A S G N C D R L T G R C L AAGTGCATCCACAACACGCTGGGGTCCACTGTGACCAGTGCAAAGCAGGCTACTATGGGGACCCGTTGGCTCCCAATCCAGCAGACAAG 1710 KCIHNTAGVHCDQCKAGYYGDPLAPNPADK 570 TGTCGAGCTTGCAACTGCAACCCAGTGGGCTCGGAGCCTGTGGAGTGTCGAAGTGATGGCAGCTGTTTTGCAAGCCAGGCTTTGGTGGC 1800 CRACNCNPVGSEPVECRSDGSCVCKPGFGG00

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GAC	CTC	3GA	AGA	GAG	GGC	ACA'	rcg	GCA	GAA	GGG	CCA	CCT	CCG'	TTT	CCT	GGA	GAC.	rag	CAT	AGA'	TGGC	TAE	rcto	GC:	rga:	CTC	AAE	3AAC	CCTG	3510
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GAG	JAAC	CAT	CAG	GGA	CAA	CCT	GCC	CCC	GGG	CTG	CTA	CAA	TAC	CCA	GGC	TCT	TGA	GCA	ACA	Gta	aaqo	tq	ccti	aqa	agat	tt	ctca	aaco	caaq	3600
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1 WPALWLSCWICFSLLLPAARATSEREVCDCNGKSRQCIFDQELHKQTGNGFRCLNCNDNTDGIHCERCKAGFYRORERDRCLPCNCNSKGSLSARCDNSG	101 RCSCKPGVTGDRCDRCLPGFHHUTDAGCAGDQRLLDSKCDCDPAGISGPCDSGRCVCKPAVTGBRCDRCRPGYYHLDGGNPQGCTQCFCYGHSASCHSSG	201 DYSVHKI <mark>ISB</mark> FHQDVDGWKAVQRNGSPAKLQMSQRHRDIFSSARRSDPVYFVAPAKFLGNQQVSYGQSLSFDYRVDRGGRHPSAHDVILEGAGLRITAPL	301 MPLSKTLPCGITKTYTFRLMEHPSSNWSPQLSYFEYRRLLRNLTALR-IRATYGEYSTCYIDNVTLISARPVSGAPAPWVEQCYCPVGYKGQFCQDCASG	400 YKRDSARLGPFGTCIPCNCQGGGACDPDTGDCYSGDENP <mark>DIP</mark> ECADCPIGFYNDP <mark>O</mark> DPRSCKPCPC <u>PNGFSCSVMPETEEVVCNNCP<mark>O</mark>GVTGARCELCAD</u>	500 GYFGDPFGERGPVRPCQPCQCUNNVDPSASGNCDRLTGRCLKCIHNTAGY#GDQCKAGY%GDPLAPNPADKCRACNCNPYGSEPVECRSDGSCVCKPGFG	600 GLSCEHAALTSCPACYNQVKWQWDQFWQQLQFLEALISKAQGGAVPNAELEGRWQQAEQALRDILREAQISQDAVRSFNLRYAKARTQENSYRDRLD	697 DLKWTVERVRALGSQYQNQVQDTRRLITQWRLSLESEASLONTNIPRSEHYVGPNGFKSLAQEATRLADSHVQSASNMEQLAKETQEYSKELMSLVRBA	797 L <mark>OBGGGSGSLDGAVVQR</mark> LVGKLQKTKSLAQELSREATQ <mark>H</mark> DMBADRSYQHSLHLLMSVSQIQGVM <mark>DQSL</mark> QVEAKR-LKQKADSLSN <mark>R</mark> VTKHMDEFKHVQ	894 SNLGNWEBETRQLLQNGKNGRQTSDQLLSRANLAKSRAQEALSMGNATFYEVENILKNLREFDLQVGDKRAEABEAMKRLSYISQKVAGASDKTRQAEAA	994 IGSAAADAQRAKNAAREALEIS <mark>GK</mark> IEQEIGELNIEANVTADGALAMEKGLATLKSEMREVEGELSRKEQEFDWDMDAVQMVIABAQRVENRAKNAGVTIQ	94 DTLNTLDGILHLIDQPGSVDEBRLILLEQKLFRAKTQINSQLRPLMSELEBRAHRQKGHLRBLETSIDGILADVKNLENIRDNLPPGCYNTQALEQQ
1 MPALWLECCLCFSLLLPAARATSRREVCDCNGKSRQCIFDRELHRQTGNGFRCLNCNDNTDGIHCEKCKAGFYRHRERDRCLPCNCNSKGSLSARCDNSG	101 RCSCKPGVTGARCDRCLPGFHMLTDAGCTQDQRLLDSKCDCDPAGIAGPCDAGGRCVCKPAVTGBRCDRCRGGYYMLDGGNPEGCTQCFCYGHSASCASSA	201 ÉYSVHKITSTFHQDVDGWKAVQRNGSPAKLQMSQRHQDVFSSAQREDPVYFVAPAKFLGNQQVSYGQSLSFDYRVDRGGRHPSAHDVILEGAGIRITAPL	301 MPLGKTLPCGITKTYTFRLMEHPSNWSPQLSYFEYRRLLRNLTALR-IRATYGEYSTCYIDNVTLISARPVSGAPAPWVEQCICPVGYKGQFCQDCASG	400 YKRDSARLGPFGTCIPCNCQGGGACDPDTGDCYSGDENPDI—ECADCPIGFYNDPHDPRSCKPCPCHNGFSCSVMPETEEVVCNNCPPGVTGARCELCAD	499 GYFGDPFGEHGPVRPCQPCQCNNNVDPSASGNCDRLTGRCLKCIHNTAGY*CDQCKAGY*FGDPLAPNPADKCRACNCNPWGSEPVGCRSDG#CVCKPGFG	599 GFNCEHĞABS-CPACYNQVKIQWDQFMQQLQRWBALISKAQGGDG-VVPDTELEGRWQQAEQALQDILRDAQISEGASRSTGFQLAKVRSQENSYGSRLD	697 DLKWTVERVRALGSQYQNRVRDTHRLITQWQLSLABSEBASLONTNIPASBHYVGPNGFKSLAQEATRLAESHVDSASNMEQLAREDYSKQALSLYRKA	797 LHEGVG <mark>S</mark> GSGSPDGAVVQGLVEKLEKTKSLAQQLÄREATQABIEADRSYQHSLRLLDSVSRLQGVSDQSFQVEEAKRIÄGKADSLSTLVTRHMDEFKRTQ	897 KNLGNWKEBAQQLLQNGKSGREKSDQLLSRANLAKSRAQEALSMGNATFYEVESILKNLREFDLQVDNKKAEABEAMKRLSYISQKVEDASDKTQQAERA	997 IGSAAADAQRAKNGAGEALEISSEIEQEIGSINIEANVTADGALAMEKGLAĞIKSEMREVEGELB ^E RKELEFDTĞMDAVQMVITBAQKYDIRAKNAGVTIQ	97 DTLNTLDGILHLBDQPLSVDEBGLYLLEQKLSRAKTQINSQLRPBMSELEBRARQQRGHLHLLETSIDGILADVKNLENIRDNLPPGCYNTQALEQQ
1 MPALWLSCCLGVALLLPASQATSRREVCDCNGKSRQCVFDQELHRQAGSGFRCLNCNDNTNGVHCERSKBGFYOHOSKGRCLPCNCHSKGSLSAGCDNSG	101 QCRCKPGVTGQRCDGCQPGPHMLTDAGCTRDQGCLDSKCDCDPAGISGPCDSGRCVCKPAVTGBRCDRCRPRDYHLDRANPEGCTQCFCYGHSASCHASA	201 DÉSVHKITSTFSQDVDGWKAVQRNGÄPAKLHWSQRHRDVFSSARRSDPVYFVAPAKFLGNQQVSYGQSLSFDYRVDRGGR <mark>Q</mark> PSA <mark>W</mark> DVILEGAGL <mark>QIR</mark> APL	301 MAPGKTLPCGITKTYTFRLMEHPSSHWSPQLSYFEYRRLLRNLTALL <mark>MIR</mark> ATYGEYSTCYIDNVTLWSARPVU <mark>R</mark> GAPAPWVE <mark>R</mark> CVGILGYKGQFCQECASG	401 YKRDSARLGAFGACWPCNCQGBGACDPDTGDCYSGDENPDI—ECADCPIGFYNDPHDPRSCKPCPCHNGFSCSVMPETEEVVCNNCPPGVTGARCELCAD	500 GPFGDPFGEHGPVRPCGRCQCNNNVDPNASGNCDQLTGRCLKCIYNTAGYYCDQCKAGYFGDPLAPNPADKCRACNCSPWGAEPFGEGGGSCVCKPGFG	600 AFNCDHAALTSCPACYNQVKIQMDQFTQQLQSLEALVSKAQGGGGGGTVPVQLEGRTBQAEQALQDILGEAQISEGAMRĀVAVRLAKARSQENDYKTRLD	700 DLKWTMERFRALGSQHQNRVQDTSRLISQWRLSLAGSEALLIBNTNIHSSEHYVGPNDFKSLAQEATRKADSHMESANAWMQLARETEDYSKQALSLARK	800 LSGGGGSGSWDSGVVQGLMGKLEKTKSLÄGQLSLEGTQADIEADRSYQHSLRLLDSASQLQGVSDTSFQVEAKR-IRQKADSLSNLVTRQTDAFTRVR	897 NNLGNWEKSTRQLLQTGKDRRQTSDQLLSRANLAKNRAQEALSMGNATFYEVENILKNLREFDLQVEDRKAEABEAMKRLSSISQKVADASDKTQQAETA	997 IGSATAD <mark>T</mark> QRAKNAAREALEISSEIE <mark>L</mark> BIGSINIEANVTADGALAMEKG <mark>T</mark> ATLKSEMREĞI <mark>-</mark> ELARKELEFDTDKDTVITEAQQADARATSAGOTIQ	96 DTLNTLDGILHLIDQPGSVDEBGMMLLEQGLFQAKTQINSRLRPLMSÜLEBRVRRQRNHLHLLETSIDGILADVKNLENIRDNLPPGCYNTQALEQQ
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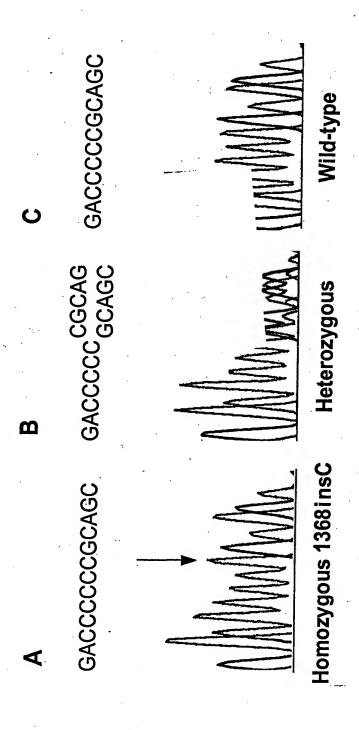


FIG. 5

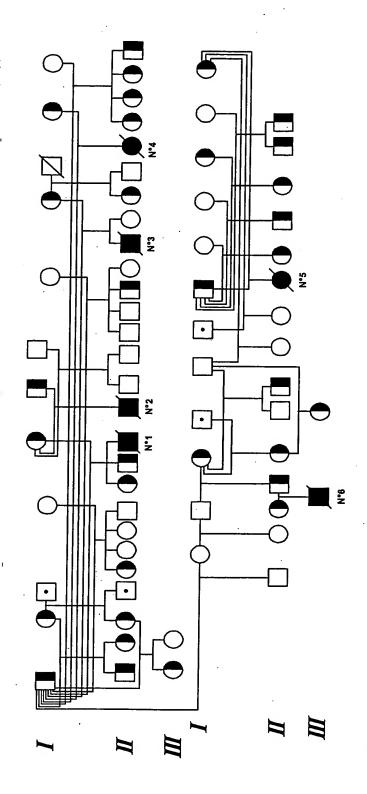


FIG. 6